

RESULT 1

A26772

Photinus-luciferin 4-monooxygenase (ATP-hydrolysing) (EC 1.13.12.7) [similarity] - com

N;Alternate names: firefly luciferase

C;Species: Photinus pyralis (common eastern firefly)

C;Date: 19-Nov-1988 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C;Accession: A26772

R;de Wet, J.R.; Wood, K.V.; DeLuca, M.; Helinski, D.R.; Subramani, S.

Mol. Cell. Biol. 7, 725-737, 1987

A;Title: Firefly luciferase gene: structure and expression in mammalian cells.

A;Reference number: A26772; MUID:87144243; PMID:3821727

A;Accession: A26772

A;Molecule type: DNA

A;Residues: 1-550

A;Cross-references: UNIPROT:P08659; UNIPARC:UPI0000038BE4; GB:M15077; NID:g160793; PID

A;Note: the authors translated the codon CAA for residue 134 as Glu

C;Comment: This protein catalyzes the oxidation of luciferin in the presence of ATP, o

C;Genetics:

A;Introns: 42/3; 112/1; 223/2; 330/2; 448/3; 504/1

C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

C;Keywords: ATP; luminescence; monooxygenase; oxidoreductase

F;71-535/Domain: acetate-CoA ligase homology

F;548-550/Region: peroxisome/glyoxysome location signal (S-[RKH]-L) motif

Alignment Scores:

Pred. No.:	6.44e-170	Length:	550
Score:	2806.00	Matches:	544
Percent Similarity:	99.6%	Conservative:	1
Best Local Similarity:	99.5%	Mismatches:	2
Query Match:	82.9%	Indels:	0
DB:	1	Gaps:	0

US-10-664-341-72 (1-1830) x A26772 (1-550)

Qy	1	ATGGCCGATGCTAAGAACATTAAGAAGGGCCCTGCTCCCTTCTACCCCTCTGGAGGATGGC	60
Db	1	MetGluAspAlaLysAsnIleLysLysGlyProAlaProPheTyrProLeuGluAspGly	20
Qy	61	ACCGCTGGCGAGCAGCTGCACAAGGCCATGAAGAGGTATGCCCTGGTGCCTGGCACCATT	120
Db	21	ThrAlaGlyGluGlnLeuHisLysAlaMetLysArgTyrAlaLeuValProGlyThrIle	40
Qy	121	GCCTTCACCGATGCCCACATTGAGGTGGACATCACCTATGCCGAGTACTTCGAGATGTCT	180
		:::	
Db	41	AlaPheThrAspAlaHisIleGluValAsnIleThrTyrAlaGluTyrPheGluMetSer	60
Qy	181	GTGCGCCTGGCCGAGGCCATGAAGAGGTACGGCCTGAACACCAACCACCGCATCGTGGTG	240
Db	61	ValArgLeuAlaGluAlaMetLysArgTyrGlyLeuAsnThrAsnHisArgIleValVal	80
Qy	241	TGCTCTGAGAACTCTCTGCAGTTCTTCATGCCAGTGCTGGGCGCCCTGTTTCATCGGAGTG	300
Db	81	CysSerGluAsnSerLeuGlnPhePheMetProValLeuGlyAlaLeuPheIleGlyVal	100
Qy	301	GCCGTGGCCCCCTGCTAACGACATTTACAACGAGCGGAGCTGCTGAACAGCATGGGCATT	360
Db	101	AlaValAlaProAlaAsnAspIleTyrAsnGluArgGluLeuLeuAsnSerMetAsnIle	120
Qy	361	TCTCAGCCTACCGTGGTGTTCGTGTCTAAGAAGGGCCTGCAGAAGATCCTGAACGTGCAG	420
Db	121	SerGlnProThrValValPheValSerLysLysGlyLeuGlnLysIleLeuAsnValGln	140

Qy	421	AAGAAGCTGCCTATCATCCAGAAGATCATCATCATGGACTCTAAGACCGACTACCAGGGC	480
Db	141	LysLysLeuProIleIleGlnLysIleIleIleMetAspSerLysThrAspTyrGlnGly	160
Qy	481	TTCCAGAGCATGTACACATTCGTGACATCTCATCTGCCTCCTGGCTTCAACGAGTACGAC	540
Db	161	PheGlnSerMetTyrThrPheValThrSerHisLeuProProGlyPheAsnGluTyrAsp	180
Qy	541	TTCGTGCCAGAGTCTTTTCGACAGGGACAAAACCATTGCCCTGATCATGAACAGCTCTGGG	600
Db	181	PheValProGluSerPheAspArgAspLysThrIleAlaLeuIleMetAsnSerSerGly	200
Qy	601	TCTACCGGCCTGCCTAAGGGCGTGGCCCTGCCTCATCGACCGCCTGTGTGCGCTTCTCT	660
Db	201	SerThrGlyLeuProLysGlyValAlaLeuProHisArgThrAlaCysValArgPheSer	220
Qy	661	CACGCCCGCGACCCCTATTTTCGGCAACCAGATCATCCCCGACACCGCTATTCTGAGCGTG	720
Db	221	HisAlaArgAspProIlePheGlyAsnGlnIleIleProAspThrAlaIleLeuSerVal	240
Qy	721	GTGCCATTCCACCACGGCTTCGGCATGTTCCACCACCTGGGCTACCTGATTTGCGGCTTT	780
Db	241	ValProPheHisHisGlyPheGlyMetPheThrThrLeuGlyTyrLeuIleCysGlyPhe	260
Qy	781	CGGGTGGTGCTGATGTACCGCTTCGAGGAGGAGCTGTTCCCTGCGCAGCCTGCAAGACTAC	840
Db	261	ArgValValLeuMetTyrArgPheGluGluGluLeuPheLeuArgSerLeuGlnAspTyr	280
Qy	841	AAAATTCAGTCTGCCCTGCTGGTGCCAACCCTGTTTCAGCTTCTTCGCTAAGAGCACCTG	900
Db	281	LysIleGlnSerAlaLeuLeuValProThrLeuPheSerPhePheAlaLysSerThrLeu	300
Qy	901	ATCGACAAGTACGACCTGTCTAACCTGCACGAGATTGCCTCTGGCGGCGCCCCACTGTCT	960
Db	301	IleAspLysTyrAspLeuSerAsnLeuHisGluIleAlaSerGlyGlyAlaProLeuSer	320
Qy	961	AAGGAGGTGGGCGAAGCCGTGGCCAAGCGCTTTCATCTGCCAGGCATCCGCCAGGGCTAC	1020
Db	321	LysGluValGlyGluAlaValAlaLysArgPheHisLeuProGlyIleArgGlnGlyTyr	340
Qy	1021	GGCCTGACCGAGACAACCAGCGCCATTCTGATTACCCAGAGGGCGACGACAAGCCTGGC	1080
Db	341	GlyLeuThrGluThrThrSerAlaIleLeuIleThrProGluGlyAspAspLysProGly	360
Qy	1081	GCCGTGGGCAAGGTGGTGCCATTCTTCGAGGCCAAGGTGGTGGACCTGGACACCGGCAAG	1140
Db	361	AlaValGlyLysValValProPhePheGluAlaLysValValAspLeuAspThrGlyLys	380
Qy	1141	ACCCTGGGAGTGAACCAGCGCGGCGAGCTGTGTGTGCGCGGCCCTATGATTATGTCCGGC	1200
Db	381	ThrLeuGlyValAsnGlnArgGlyGluLeuCysValArgGlyProMetIleMetSerGly	400
Qy	1201	TACGTGAATAACCCTGAGGCCACAAACGCCCTGATCGACAAGGACGGCTGGCTGCACTCT	1260
Db	401	TyrValAsnAsnProGluAlaThrAsnAlaLeuIleAspLysAspGlyTrpLeuHisSer	420
Qy	1261	GGCGACATTGCCTACTGGGACGAGGACGAGCACTTCTTCATCGTGACCGCCTGAAGTCT	1320
Db	421	GlyAspIleAlaTyrTrpAspGluAspGluHisPhePheIleValAspArgLeuLysSer	440

Qy	1321	CTGATCAAGTACAAGGGCTACCAGGTGGCCCCAGCCGAGCTGGAGTCTATCCTGCTGCAG	1380
Db	441	LeuIleLysTyrLysGlyTyrGlnValAlaProAlaGluLeuGluSerIleLeuLeuGln	460
Qy	1381	CACCCTAACATTTTCGACGCCGGAGTGGCCGGCCTGCCCGACGACGATGCCGGCGAGCTG	1440
Db	461	HisProAsnIlePheAspAlaGlyValAlaGlyLeuProAspAspAspAlaGlyGluLeu	480
Qy	1441	CCTGCCGCCGTCGTCGCTGGAACACGGCAAGACCATGACCGAGAAGGAGATCGTGGAC	1500
Db	481	ProAlaAlaValValValLeuGluHisGlyLysThrMetThrGluLysGluIleValAsp	500
Qy	1501	TATGTGGCCAGCCAGGTGACAACCGCCAAGAAGCTGCGCGGCGGAGTGGTGTTCGTGGAC	1560
Db	501	TyrValAlaSerGlnValThrThrAlaLysLysLeuArgGlyGlyValValPheValAsp	520
Qy	1561	GAGGTGCCCAAGGGCCTGACCGGCAAGCTGGACGCCCGCAAGATCCGCGAGATCCTGATC	1620
Db	521	GluValProLysGlyLeuThrGlyLysLeuAspAlaArgLysIleArgGluIleLeuIle	540
Qy	1621	AAGGCTAAGAAAGGCGGCAAG	1641
Db	541	LysAlaLysLysGlyGlyLys	547